

## Chem 464 Biochemistry

*Multiple choice (4 points apiece):*

1. In the binding of oxygen to myoglobin, the relationship between the concentration of oxygen and the fraction of binding sites occupied can best be described as:  
A) hyperbolic.  
B) linear with a negative slope.  
C) linear with a positive slope.  
D) random.  
E) sigmoidal
2. Which one of the following statements is true of enzyme catalysts?  
A) They bind to substrates, but are never covalently attached to substrate or product.  
B) They increase the equilibrium constant for a reaction, thus favoring product formation.  
C) They increase the stability of the product of a desired reaction by allowing ionizations, resonance, and isomerizations not normally available to substrates.  
D) They lower the activation energy for the conversion of substrate to product.  
E) To be effective they must be present at the same concentration as their substrates.
3. The steady state assumption, as applied to enzyme kinetics, implies:  
A)  $K_m = K_s$ .  
B) the enzyme is regulated.  
C) the ES complex is formed and broken down at equivalent rates.  
D) the  $K_m$  is equivalent to the cellular substrate concentration.  
E) the maximum velocity occurs when the enzyme is saturated.
4. Which of following is an anomeric pair?  
A) D-glucose and D-fructose  
B) D-glucose and L-fructose  
C) D-glucose and L-glucose  
D)  $\alpha$ -D-glucose and  $\beta$ -D-glucose  
E)  $\alpha$ -D-glucose and  $\beta$ -L-glucose
5. The biochemical property of lectins that is the basis for most of their biological effects is their ability to bind to:  
A) amphipathic molecules.  
B) hydrophobic molecules.  
C) specific lipids.  
D) specific oligosaccharides.  
E) specific peptides.

6. The difference between a ribonucleotide and a deoxyribonucleotide is:
- A) a deoxyribonucleotide has an —H instead of an —OH at C-2.
  - B) a deoxyribonucleotide has  $\alpha$  configuration; ribonucleotide has the  $\beta$  configuration a C-1.
  - C) a ribonucleotide has an extra —OH at C-4.
  - D) a ribonucleotide has more structural flexibility than deoxyribonucleotide.
  - E) a ribonucleotide is a pyranose, deoxyribonucleotide is a furanose.
7. In living cells, nucleotides and their derivatives can serve as:
- A) carriers of metabolic energy.
  - B) enzyme cofactors.
  - C) intracellular signals.
  - D) precursors for nucleic acid synthesis.
  - E) all of the above.

*Essay Questions 10 points each*

8. What is the Bohr effect and why is it important in the binding of oxygen to hemoglobin?

**Bohr Effect - effect of pH and CO<sub>2</sub> on O<sub>2</sub> binding to hemoglobin**

H<sup>+</sup> and O<sub>2</sub> bound at different sites (O<sub>2</sub> heme and His<sup>146</sup> (HC3) on  $\beta$  subunit His HC3 when protonated it makes a salt bridge with Asp 94 . This bridge stabilizes the T state with lower affinity for O<sub>2</sub>. so at pH $\downarrow$  [H<sup>+</sup>] $\uparrow$  this gets ionized, T form stabilized, O<sub>2</sub> affinity lowered, O<sub>2</sub> released.

CO<sub>2</sub> can do the same thing.

CO<sub>2</sub> $\uparrow$ , carbonic anhydrase changes to H<sub>2</sub>CO<sub>3</sub>, pH $\downarrow$  have above effect but in addition CO<sub>2</sub> binds to hemoglobin as a carbamate on the NH<sub>2</sub> terminal of all for hemoglobin molecules

This makes amino terminal negatively charged instead of positively charged.

This, in turn, makes an additional salt bridge that stabilizes the T state to lower the affinity for O<sub>2</sub> and release more O<sub>2</sub> from hemoglobin

9. Define the following terms and explain how they can be used by an enzyme to increase the rate of a reaction

Induced fit

Entropy Reduction

Desolvation

Induced fit - Enzyme undergoes a conformational change when a substrate binds. This conformation change can be used to bring critical catalytic residues into proper position for reaction or can be used to help shield transition state from other chemicals in the system that could interfere with the reaction.

Entropy Reduction - Restriction of the movement of substrate, holding the substrate in one place and aligning it properly through many weak interactions the enzyme limits the substrate to a conformation where the reaction can occur, and prevents it from assuming other conformations that cannot react or that would take a higher energy to react.

Desolvation - Weak enzyme substrate interactions can replace many of the substrate solvent interactions and, essentially take the substrate out of solution. This is necessary because water can interfere in many reactions to produce incorrect products. And some reactions that are hydrophobic by nature cannot be performed in an aqueous environment

10. One of the way of analyzing enzyme kinetics is to plot  $v_o$  vs  $[S]$ . Make a sketch of a plot like this and determine  $K_m$  and  $V_{max}$  from the data in your plot.

Sketch similar to figure 6-11 or 6-12. Either showing the points that give you  $V_{max}$  and  $K_m$  or preferably including numbers on X and Y axes and giving a hard number for these parameters based on plot

11. Compare and contrast the structure of starch and glycogen

Both are polymers of glucose residues connected by primarily ( $\alpha$ 1-4) linkages

Starch is actually 2 polymers

Amylose - with linear ( $\alpha$ 1-4) linkages

Amylopectin with the same ( $\alpha$ 1-4) linkage backbone but occasional ( $\alpha$ 1-6) branch points. Branches occur about every 24- 30 residues)

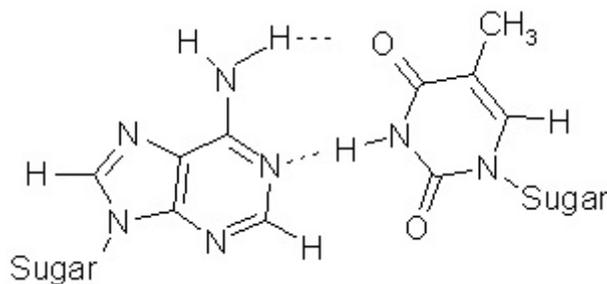
Extensive hydrogen bonding between sugars and solvent and make for a complicated and very hydrated overall structure.

Glycogen is like amylopectin; linear ( $\alpha$ 1-4) with ( $\alpha$ 1-6) branch points, but branch points are more frequent about every 8-12 residues. Also very hydrated structure

12. Briefly discuss proteoglycans, include relative size of protein and carbohydrate, where any why they are used in an organism, some example molecules and some observed structural features.

Proteoglycans - macromolecules of cell surface or extracellular matrix. Most of the mass is carbohydrate. Basic proteoglycan consists of a core protein with attached carbohydrate. Had two examples in lecture notes and book. One (figure 7-27) is a membrane protein with either long heparin sulfate for chondroitin sulfate carbohydrate chains attached at Gly-X-Gly-Ser sequences, the other (Figure 7-29) is a proteoglycan aggregate consisting of many Aggrecan core proteins (Molar mass  $\sim 250,000$ ) attached to a single hyaluronate, and each aggrecan is in turn linked to multiple chondroitin sulfate and keratan sulfates to give a total molar mass  $>2 \times 10^8$

13. Sketch the structure of A hydrogen-bonded to T



14. What is hypochromism and how does it relate to the melting of DNA

Hypochromism refers to the fact that DNA has a lower absorbance at 260 nm that you would calculate based on the sum of the absorbancies of the monomers. This occurs because the bases stacked in the core of the helix have electronic interactions with the bases above and below them that change their light absorbing properties. This hyperchromism disappears when DNA is denatured. This make observing DNA absorbance at 260 nm a good way to follow DNA melting or denaturation. Essential the absorbance at 260nm will increase about 30% when DNA is denatured

**Alternate question for those who did the assigned problems. Can be substituted for any 10 point question.**

The cells of many eukaryotic organisms have highly specialized systems that repair G-T mismatches in DNA. The mismatch is repaired to G·C not A·T. This mismatch repair system occurs in addition to the more general system that repairs virtually all mismatches. Can you suggest why cells might require a specialized system to repair G-T mismatches?

About 5% of the C found in eukaryotic cells is methylated to 5-methyl C. When 5-Methyl C undergoes spontaneous deamination it becomes T. Thus this is one of the most common mismatches found in Eukaryotic cells, and the easiest to evolve (design) a repair system around, since the odds are great when you find a G-T mismatch that it is the T that is wrong, not the G.